
Preferential biological processes in the human limbus by differential gene profiling.

Journal: PLoS One

Publication Year: 2013

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PubMed link: 23630617

Funding Grants: Regeneration of Functional Human Corneal Epithelial Progenitor Cells

Public Summary:

Corneal epithelial stem cells or limbal stem cells (LSCs) are responsible for the maintenance of the corneal epithelium in humans. The exact location of LSCs is still under debate, but the increasing need for identifying the biological processes in the limbus, where LSCs are located, is of great importance in the regulation of LSCs. In our current study we identified 146 preferentially expressed genes in the human limbus in direct comparison to that in the cornea and conjunctiva. The expression of newly identified limbal transcripts endomucin, fibromodulin, paired-like homeodomain 2 (PITX2) and axin-2 were validated using qRT-PCR. Further protein analysis on the newly identified limbal transcripts showed protein localization of PITX2 in the basal and suprabasal layer of the limbal epithelium and very low expression in the cornea and conjunctiva. Two other limbal transcripts, frizzled-7 and tenascin-C, were expressed in the basal epithelial layer of the limbus. Gene ontology and network analysis of the overexpressed limbal genes revealed cell-cell adhesion, Wnt and TGF-beta/BMP signaling components among other developmental processes in the limbus. These results could aid in a better understanding of the regulatory elements in the LSC microenvironment.

Scientific Abstract:

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